



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Morris Reichlin and Eugen Koren
- (ii) TITLE OF INVENTION: METHOD FOR TREATMENT OF SLE

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

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1201 West Peachtree Street
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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/800,682
- (B) FILING DATE: 14-FEB-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US96/07597
- (B) FILING DATE: 24-MAY-1996
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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- (B) REGISTRATION NUMBER: 31,284
- (C) REFERENCE/DOCKET NUMBER: OMRF 158 CIP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

GGTGAAGAAG GAGTTGTGCC AGCACGTGAG TACTCAGACG ATCGTAACAT CAACCTGGCA	60
GACGAATTAA AAATTGGTGA TACCATTGAA GCAGTTGTCA TTTCTAACGT AACAAAGCGAC	120
AAGGAAGGCG TCAGTTACTT GTGTCAAAG AAGCGTTGG ATGCGCGCAA GGCATGGAA	180
AACTTGAGCT TTGCTGAAGG TGACACAGTT GATGCCAAGG TTATCAACGC TGTCGTGGT	240
GGTTTGATTG TTGATGTTAA CGGCGTACGT GGTTTGTAC CAGCATCAAT GGTTGCAGAA	300
CGTTTCGTTT CTGATTGAA CCAATTCAAG AATAAGGATA TTAAAGCACA AGTTATCGAA	360
ATTGACCCCTG CTAATGCACG TTTGATTTG TCACGTAAGG CTGTTGCTGC ACAAGAACGC	420
GCTGCACGAT TGGCTGAAGT ATTTAGCAAG TTGTCAGTTC GTGAAGTTGT TGAAGGAACT	480
GTTGCCCGTT TGACAGACTT CGGCGCATTG GTTGACTTGG GTGGTGTGA TGGTTGGTT	540
CACGTATCAG AAATCTCACA CGATCGTGTG AAGAACCCGG CCGATGTATT GACAAAGGGT	600
GACAAGGTTG ATGTTAAGAT CTTGGCATTG GACACTGAAA AGGGTCGTAT CTCATTGTCA	660
ATCAAAGCAA CACAACGTGG ACCTTGGGAC GAAGCTGCAG ATCAAATCGC TGCAGGTTCA	720
G TGCTTGAAG GTACTGTTAA GCGTGTGAAG GACTTGGTG CCTTTGTGA AATTTGCCT	780
GGTATCGAAG GTCTTGTGCA CGTGTACAA ATTCAAACA AGCGTATTGA AAACCCATCA	840
GAAGTTTGA AGTCTGGTGA CAAGGTACAA GTGAAGGTAT TGGACATTAA GCCAGCCGAA	900
GAACGTATTT CATTGTCAAT GAAGGCTTG GAAGAAAAGC CAGAACGTGA AGATCGTCGT	960
GGTAACGATG GTTCAGCTTC ACGTGCTGAT ATCGCTGCTT ACAAGCAACA AGATGACTCA	1020
GCCGCAACAT TGGGTGACAT CTTGGTGAT AAGTTGTAAG AGGCATCAAC ATAAAAGAGC	1080
TGGTCGCCA GTTCTTTAT TTTTGAAGAA AAATTGAGTG GGCATTAGTG GGCGCTCACG	1140
GTATGAAAAA GGAGGTGCGA TTATGGCAGC ACCAGTAGTA GCCATTGTTG GCGACCAAAC	1200
GTCGGAAAAT CGACTATCTT TAACCGGATG GCCGGAGAAC GTATTGCAAT TGTTGAAGAT	1260
CAACCAGGGG TAACACCGCGA TCGTTGTAC GCGCCAGCCG AATGGTTGAA TTAT	1314

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Gly Glu Glu Gly Val Val Pro Ala Arg Glu Tyr Ser Asp Asp Arg Asn

1 5 10 15
Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu Ala Val
20 25 30
Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser Tyr Leu Leu
35 40 45
Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu Asn Leu Ser Phe
50 55 60
Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val Arg Gly
65 70 75 80
Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro Ala Ser
85 90 95
Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys Asn Lys
100 105 110
Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala Arg Leu
115 120 125
Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala Gln Leu
130 135 140
Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu Gly Thr
145 150 155 160
Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val
165 170 175
Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val Lys Asn
180 185 190
Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys Ile Leu
195 200 205
Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys Ala Thr
210 215 220
Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala Gly Ser
225 230 235 240
Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala Phe Val
245 250 255
Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln Ile Ser
260 265 270
Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly Asp Lys
275 280 285
Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Glu Arg Ile Ser
290 295 300
Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu Asp Arg Arg

305 310 315 320

Gly Asn Asp Gly Ser Ala Ser Arg Ala Asp Ile Ala Ala Tyr Lys Gln
325 330 335

Gln Asp Asp Ser Ala Ala Thr Leu Gly Asp Ile Phe Gly Asp Lys Leu
340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val
1 5 10 15

Arg Gly Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro
20 25 30

Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys
35 40 45

Asn Lys Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala
50 55 60

Arg Leu Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala
65 70 75 80

Gln Leu Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu
85 90 95

Gly Thr Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly
100 105 110

Gly Val Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val
115 120 125

Lys Asn Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys
130 135 140

Ile Leu Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys
145 150 155 160

Ala Thr Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala
165 170 175

Gly Ser Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala
180 185 190

Phe Val Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln
195 200 205

Ile Ser Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly
210 215 220

Asp Lys Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Glu Arg
225 230 235 240

Ile Ser Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu
245 250 255

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Ala Tyr Glu Asp Ala Glu Thr Val Thr Gly Val Ile Asn Gly Lys Val
1 5 10 15

Lys Gly Gly Phe Thr Val Glu Leu Asp Gly Ile Arg Ala Phe Leu Pro
20 25 30

Gly Ser Leu Val Asp Val Arg Pro Val Arg Asp Thr Leu His Leu Glu
35 40 45

Gly Lys Glu Leu Glu Phe Lys Val Ile Lys Leu Asp Gln Lys Arg Asn
50 55 60

Asn Val Val Val Ser Arg Arg Ala Val Ile Glu Ser Glu Asn Ser Ala
65 70 75 80

Glu Arg Asp Gln Leu Leu Glu Asn Leu Gln Glu Gly Met Glu Val Lys
85 90 95

Gly Ile Val Lys Asn Leu Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly
100 105 110

Gly Val Asp Gly Leu Leu His Ile Thr Asp Met Ala Trp Lys Arg Val
115 120 125

Lys His Pro Ser Glu Ile Val Asn Val Gly Asp Glu Ile Thr Val Lys
130 135 140

Val Leu Lys Phe Asp Arg Glu Arg Thr Arg Val Ser Leu Gly Leu Lys
145 150 155 160

Gln Leu Gly Glu Asp Pro Trp Val Ala Ile Ala Lys Arg Tyr Pro Glu
165 170 175

Gly Thr Lys Leu Thr Gly Arg Val Thr Asn Leu Thr Asp Tyr Gly Cys
180 185 190

Phe Val Glu Ile Glu Glu Gly Val Glu Gly Leu Val His Val Ser Glu
195 200 205

Met Arg Asp Arg Val Glu Asp Ala Thr Leu Val Leu Ser Val Gly Asp
210 215 220

Glu Val Glu Ala Lys Phe Thr Gly Val Asp Arg Lys Asn Arg Ala Ile
225 230 235 240

Ser Leu Ser Val Arg Ala Lys Asp Glu Ala Asp Glu Lys Asp
245 250

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Lys Phe Glu Ala Gly Glu Arg Val Glu Gly Ile Ile Phe Asn Gln Val
1 5 10 15

Lys Gly Gly Phe Thr Val Asp Leu Asp Gly Ala Val Ala Phe Leu Pro
20 25 30

Arg Ser Gln Val Asp Ile Arg Pro Ile Arg Asp Val Thr Pro Ala Asp
35 40 45

Ala Gln Pro Ala Ala Leu Arg Asn Leu Lys Met Asp Lys Arg Arg Gly
50 55 60

Asn Ile Val Val Ser Arg Arg Thr Val Leu Glu Glu Ser Arg Ala Glu
65 70 75 80

Gln Arg Ser Glu Ile Val Gln Asn Leu Glu Glu Gly Gln Val Val Glu
85 90 95

Gly Val Val Lys Asn Ile Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly
100 105 110

Gly Ile Asp Gly Leu Leu His Val Thr Asp Met Ala Trp Arg Arg Val
115 120 125

Lys His Pro Ser Glu Ile Gln Asn Ile Gly Gln Gln Val Lys Val Gln
130 135 140

Ile Ile Arg Ile Asn Gln Glu Thr His Arg Ile Ser Leu Gly Met Lys
145 150 155 160

Gln Leu Glu Ser Asp Pro Trp Asp Gly Ile Gly Ala Lys Tyr Pro Val
165 170 175

Gly Lys Lys Ile Ser Gly Thr Val Thr Asn Ile Thr Asp Tyr Gly Ala
180 185 190

Phe Val Glu Leu Glu Pro Gly Ile Glu Gly Leu Ile His Ile Ser Glu
195 200 205

Met Asn Arg Pro Gly Glu Gln Val Ile Glu Glu Phe Asn Lys Gly Asp
210 215 220

Val Val Arg Ala Val Val Leu Asp Val Asp Val Asp Lys Glu Arg Ile
225 230 235 240

Ser Leu Gly Ile Lys Gln Leu
245

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

Glu Thr Val Thr Gly Val Ile Asn Gly Lys Val Lys Gly Gly Phe Thr
1 5 10 15

Val Glu Leu Asn Gly Ile Arg Ala Phe Leu Pro Gly Ser Leu Val Asp
20 25 30

Val Arg Pro Val Arg Asp Thr Thr His Leu Glu Gly Lys Glu Leu Glu
35 40 45

Phe Lys Val Ile Lys Leu Asp Gln Lys Arg Asn Asn Val Val Val Ser
50 55 60

Arg Arg Ala Val Ile Glu Ser Glu Ser Ala Glu Arg Asp Gln Leu
65 70 75 80

Leu Glu Asn Leu Gln Glu Gly Met Glu Val Lys Gly Ile Val Lys Asn
85 90 95

Leu Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly Gly Val Asp Gly Leu
100 105 110

Leu His Ile Thr Asp Met Ala Trp Lys Arg Val Lys His Pro Ser Glu
115 120 125

Ile Val Asn Val Gly Asp Glu Ile Thr Val Lys Val Leu Lys Phe Asp
130 135 140

Arg Glu Arg Thr Arg Val Ser Leu Gly Leu Lys Gln Leu Gly Glu Asp
145 150 155 160

Pro	Trp	Val	Ala	Ile	Ala	Lys	Arg	Tyr	Pro	Glu	Gly	Thr	Lys	Leu	Thr
165									170					175	
Gly	Arg	Val	Thr	Asn	Leu	Thr	Asp	Tyr	Gly	Cys	Phe	Val	Glu	Ile	Glu
180									185					190	
Glu	Gly	Val	Glu	Gly	Leu	Val	His	Val	Ser	Glu	Met	Lys	Lys	Gly	Asp
195						200					205				
Glu	Ile	Ala	Ala	Val	Val	Leu	Gln	Val	Asp	Ala	Glu	Arg	Glu	Arg	Ile
210					215					220					
Ser	Leu	Gly	Val	Lys	Gln	Leu	Ala	Glu	Asp	Pro					
225					230			235							

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

Ala	Glu	Asp	Val	Val	Val	Lys	Gly	Lys	Ile	Val	Gly	Ala	Asn	Lys	Gly
1					5				10				15		

Gly	Val	Val	Ala	Leu	Val	Glu	Gly	Leu	Arg	Gly	Phe	Val	Pro	Phe	Ser
					20			25				30			

Gln	Ile	Ser	Ser	Lys	Ser	Ser	Ala	Glu	Glu	Leu	Glu	Lys	Glu	Ile	
					35			40			45				

Pro	Leu	Lys	Phe	Val	Glu	Val	Asp	Glu	Glu	Gln	Ser	Arg	Leu	Val	Met
					50			55			60				

Ser	Asn	Arg	Lys	Ala	Met	Ala	Asp	Ser	Gln	Ala	Met	Ala	Asp	Ser	Gln
					65			70			75			80	

Ala	Gln	Leu	Gly	Ile	Gly	Ser	Val	Val	Thr	Gly	Thr	Val	Gln	Ser	Leu
					85			90				95			

Lys	Pro	Tyr	Gly	Ala	Phe	Ile	Asp	Ile	Gly	Gly	Ile	Asn	Gly	Leu	Leu
					100			105			110				

His	Val	Ser	Gln	Ile	Ser	His	Asp	Arg	Val	Ser	Asp	Ile	Ala	Thr	Val
					115			120			125				

Leu	Gln	Pro	Gly	Asp	Thr	Leu	Lys	Val	Met	Ile	Leu	Ser	His	Asp	Arg
					130			135			140				

Glu	Arg	Gly	Arg	Val	Ser	Leu	Ser	Thr	Lys	Lys	Leu	Glu	Pro	Thr	Pro
					145			150			155			160	

Gly Asp

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Gly Thr Val

1

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Asp Phe Gly Ala Phe Val

1

5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

Gly Leu Val His Val Ser

1

5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Gly Asp Lys Val
1

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

Arg Ile Ser Leu Ser
1 5